

OM nucleic - protein search, using frame_plus_n2p model

Run on: March 18, 2004, 06:12:39 ; Search time 72.5 Seconds

(without alignments)
11658.348 Million cell updates/sec

Title: US-09-938-956-6

Perfect score: 2908

Sequence: 1 atgagacgacccggaacta.....tattogagcccttgatga 1632

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Ygapop 10.0 , Ygapext 0.5	
Zgapop 6.0 , Zgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1049977 seqs, 258955339 residues

Total number of hits satisfying chosen parameters: 209954

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=published Applications AA -QFWT=fasta -SUFFIX=rapb -MINMATCH=0.1
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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DLEXT=7

Database : Published Applications AA:*

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- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep.*
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- 10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep.*
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- 18: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description

1	2881	98.1	543	9	US-09-938-956-7	Sequence 7, Appli
2	2876	98.9	599	9	US-09-887-586A-22	Sequence 22, Appl
3	2876	98.9	599	9	US-09-903-012-22	Sequence 22, Appl
4	2876	98.9	599	10	US-09-900-797-22	Sequence 24, Appl
5	1633.5	56.2	591	9	US-09-887-586A-24	Sequence 24, Appl
6	1633.5	56.2	591	9	US-09-903-012-24	Sequence 24, Appl
7	1633.5	56.2	591	10	US-09-900-797-24	Sequence 24, Appl
8	1553.5	53.4	590	9	US-09-887-586A-54	Sequence 54, Appl
9	1553.5	53.4	590	9	US-09-903-012-54	Sequence 54, Appl
10	1553.5	53.4	590	10	US-09-900-797-54	Sequence 54, Appl
11	1468	50.5	598	9	US-09-887-586A-26	Sequence 26, Appl
12	1468	50.5	598	9	US-09-903-012-26	Sequence 26, Appl
13	1468	50.5	598	10	US-09-900-797-26	Sequence 26, Appl
14	836	28.7	556	9	US-09-887-586A-32	Sequence 32, Appl
15	836	28.7	556	9	US-09-903-012-32	Sequence 32, Appl
16	836	28.7	556	10	US-09-900-797-32	Sequence 32, Appl
17	806.5	27.7	548	9	US-09-887-586A-2	Sequence 2, Appli
18	806.5	27.7	548	9	US-09-903-012-2	Sequence 2, Appli
19	806.5	27.7	548	10	US-09-900-797-2	Sequence 8, Appli
20	804.5	27.7	548	9	US-09-887-586A-8	Sequence 12, Appl
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23	804.5	27.7	548	9	US-09-903-012-12	Sequence 12, Appl
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26	803.5	27.6	548	9	US-09-887-586A-6	Sequence 6, Appli
27	803.5	27.6	548	9	US-09-903-012-6	Sequence 6, Appli
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32	792.5	27.3	548	9	US-09-887-586A-10	Sequence 10, Appl
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38	734	25.2	548	10	US-09-900-797-52	Sequence 52, Appl
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40	714	24.6	628	9	US-09-887-586A-20	Sequence 20, Appl
41	714	24.6	628	9	US-09-903-012-20	Sequence 20, Appl
42	714	24.6	628	10	US-09-900-797-20	Sequence 20, Appl
43	714	24.6	628	13	US-10-041-007-22	Sequence 22, Appl
44	714	24.6	628	14	US-10-025-145A-4	Sequence 4, Appli
45	704.5	24.2	551	15	US-10-411-066-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-938-956-7
; Sequence 7, Application US/09938956
; Patent No. US20020142408A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Siquan
; APPLICANT: Dicosimo, Deana J.
; APPLICANT: Koffas, Mattheos
; APPLICANT: Odom, J. Martin
; TITLE OF INVENTION: Production of Monoterpene
; FILE REFERENCE: CL1809 US NA
; CURRENT APPLICATION NUMBER: US/09/938,956
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/229,907
; PRIOR FILING DATE: 2000-09-0
; PRIOR APPLICATION NUMBER: 60/229,958
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 7
; LENGTH: 543
; TYPE: PXT
; ORGANISM: Mentha spicata
US-09-938-956-7

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321 AsnSerIleAspGlnLeuProAspTyrMetGlnLeuCysPheLeuAlaLeuAsnAsnPhe 340
1021 GTCGATGATACATCGTACGATGTTATGAAGAGAGAAGCGCTCAACGTTTATACCTACCTG 1080
341 ValAspAspThrSerTyrAspValMetLysGluLysGlyValAsnValIleProTyrLeu 360
1081 CGCAATCTGGTGGTGGATTGGCGGATAGTATATGGTAGAGCGACGGTGGTTCACGGC 1140
361 ArgGlnSerTrpValAspLeuAlaAspLysTyrMetValGluAlaArgTrpPheTyrGly 380
1141 GGCACAAACCAAGTTTGAAGAGTATTTGGAGAACTCATGCGAGTCGATAGTGGGCC 1200
381 GlyHisLysProSerLeuGluGluTyrLeuGluAsnSerTrpGlnSerIleSerGlyPro 400
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RESULT 2
US-09-887-586A-22
; Sequence 22, Application US/09887586A
; Patent No. US20020094556A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094556A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/887, 586A
; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 599

Alignment Scores:
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Percent Similarity: 100.00% Conservative: 0
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Query Match: 99.07% Indels: 0
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QY 301 ACATCTCTGCTTTAGCTCTCTCAGACACATGCTTTTCAAGTCGACAGAGGATTC 360
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QY 841 GCAGGATTAATGATGGGCAAGTCAACGCTCTGATGATGATGATGATGATGATGATGATGAT 900
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TYPE: PRT
; ORGANISM: Mentha spicata
US-09-887-586A-22

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Score: 2876.00 Matches: 542
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.90% Indels: 0
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Db 298 SerPheArgTrpTrpArgAsnThrGlyPheValGluLysLeuProPheAlaArgAspArg 317
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QY 904 TATGGCACTTAGAAGAACTCGAACAATCTACTGACCTCATTCGAAGATGGATATAAC 963
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QY 1024 GATGATACATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1083
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Db 558 PheIleGlyCysAlaValAspLeuGlyArgMetAlaGlnLeuMetTyrHisAsnGlyAsp 577
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US-09-903-012-22
; Sequence 22, Application US/09903012
; Patent No. US20020094557A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094557A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262

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; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Mentha spicata
US-09-903-012-22

Alignment Scores:
Pred. No.: 5,12e-260 Length: 599
Score: 2876.00 Matches: 542
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 98.90% Indels: 0
DB: 5 Gaps: 0

US-09-938-956-6 (1-1632) x US-09-903-012-22 (1-599)
QY 4 AGAGATCCGGAACATACAAACCTCTCTGCTGGGATGTCAACTTCATCCAACTCGTCTCTC 63
Db LeuValGluCysTyrPheTrpAsnThrGlyIleGluProArgGlnHisAlaSerAla 337
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Db GlnSerTrpValAspLeuAlaAspLysTyrMetValGluAlaArgTrpPheTyrGlyGly 437
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Db 438 HieLysProSerLeuGluGluTyrLeuGluAsnSerTrpGlnSerIleSerGlyProCys 457
QY 1204 ATGTTAACGACACATATTTCTCCGAGTAAACAGATTCGTTTCAAAAGGAGACCGTCGACAGT 1263
Db 458 MetLeuThrHisIlePhePheArgValThrAspSerPheThrLysGluThrValAspSer 477
QY 1264 TTGTACAAATACCAACGATTTAGTTCGTTGCTCATCTCTGCTTCGGCTTGTCTGATGAT 1323
Db 478 LeuTyrLysTyrHisAspLeuValArgTrpSerSerPheValLeuArgLeuAlaAspAsp 497
QY 1324 TTGGAACTCCGTTGGAGAGGTGACGAGAGGGGATGTCGCGAAATCCTTCAGTGTCTAC 1383
Db 498 LeuGlyThrSerValGluValSerArgGlyAspValProLysSerLeuGlnCysTyr 517
QY 1384 ATGAGTGACTACATGATCGGAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1443
Db 518 MetSerAspTyrAsnAlaSerGluAlaGluAlaArgLysHisValLysTrpLeuIleAla 537
QY 1444 GAGGTGGAGAGAGATGAAATGCGAGAGGGGTGTCGAGAGGATTCCTCATTCGCGCAAGAT 1503
Db 538 GluValTrpLysLysMetAsnAlaGluArgValSerLysAspSerProPheGlyLysAsp 557
QY 1504 TTTATAGATGTGCGATTGATTAGGAGGATGCGCGAGGATGCGCGAGTGTGATACCATATGGAGAT 1563
Db 558 PheIleGlyCysAlaValAspLeuGlyArgMetAlaGlnLeuMetTyrHisAsnGlyAsp 577
QY 1564 GGGCAGCGCACACACACCTTATATACATCAACAAATGACCAAGATGACCAAGATGACCAAGAT 1623
Db 578 GlyHisGlyThrGlnHisProIleIleHisGlnGlnMetThrArgThrLeuPheGluPro 597
QY 1624 TTTGCA 1629
Db 598 PheAla 599

RESULT 4
US-09-900-797-22
; Sequence 22, Application US/09900797
; Publication No. US20030087406A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20030087406A1, Joseph P.
; APPLICANT: Starko, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; FILING DATE: 1999-09-17

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; PRIOR APPLICATION NUMBER: 60/130,628
 ; PRIOR FILING DATE: 1999-04-22
 ; PRIOR APPLICATION NUMBER: 60/150,262
 ; PRIOR FILING DATE: 1999-08-23
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: RastSeq for Windows Version 3.0
 ; SEQ ID NO 22
 ; LENGTH: 599
 ; TYPE: PRT
 ; ORGANISM: Mentha spicata
 US-09-900-797-22

Alignment Scores:
 Pred. No.: 5,12e-260 Length: 599
 Score: 2876.00 Matches: 542
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 98.90% Indels: 0
 DB: 10 Gaps: 0

US-09-938-956-6 (1-1632) x US-09-900-797-22 (1-599)

QY 4 AGAGATCCGGAACATAACACCTTCCTGTTGGGATGTCACATTCATCCATCGCTTCTC 63
 Db 58 ArgArgSerGlyAsnTyrAsnProSerArgTrpAspValAsnPheIleGlnSerLeuLeu 77
 QY 64 AGTACTATAAGGAGGACAAACACGTGATTAGGCTTCTGAGCTGGTCACTTTGGTGAAG 123
 Db 78 SerAspTyrLysGluAspLysHisValIleArgAlaSerGluLeuValThrLeuValLys 97
 QY 124 ATGGAATCGGAGAAAGAACCGATCAATTCGACAACTTCGATGTTGATCGATGATTCGAG 183
 Db 98 MetGluLeuGluLysGluThrAspGlnIleArgGlnLeuGluLeuIleAspAspLeuGln 117
 QY 184 AGGATGGGCTGTCGATCATTCCAAATGAGTTCAAAGAAATCTTGTCTCTATATAT 243
 Db 118 ArgMetGlyLeuSerAspHisPheGlnAsnGluPheLysGluIleLeuSerSerIleTyr 137
 QY 244 CTCGACCATCACTATTACAAACCCCTTTTCCAAAGAAAGAGGATCTCTATCCACA 303
 Db 138 LeuAspHisHisTyrTyrLysAsnProPheProLysGluGluA-GaspLeuTyrSerThr 157
 QY 304 TCTCTGATATTAGCTCCTCAGAGAACATCGTTTTCAGTCGACAAAGAGTATTCGAT 363
 Db 158 SerLeuAlaPheArgLeuLeuArgGluHisGlyPheGlnValAlaGlnGluValPheAsp 177
 QY 364 AGTTTCAGAACGAGGAGGGTGGTTCAAAGAAAGCCTTAGCGACGACACAGAGGATTG 423
 Db 178 SerPheLysAsnGluGluGlyGluPheLysGluSerLeuSerAspAspThrArgGlyLeu 197
 QY 424 TTGCAACTGTATGAGCTTCCTTCTGTTGACGAGCGGAAAGCAGCCCTCGAGTCAGCG 483
 Db 198 LeuGlnLeuTyrGluAlaSerPheLeuLeuThrGluGlyGluThrLeuGluSerAla 217
 QY 484 AGGAAATCGGCACCAAAATTTTGGAGGAAAGTGAACGAGGTTGTTGATGGCGAC 543
 Db 218 ArgGluPheAlaThrLysPheLeuGluGluLysValAsnGluGlyValAspGlyAsp 237
 QY 544 CTTTTCACAGAAATCGCATATCTTTGGACATCCCTTTCATTCGAGGATTAAAGGCCA 603
 Db 238 LeuLeuThrArgIleAlaTyrSerLeuAspIleProLeuHisTrpAspGlyLeuArgPro 257
 QY 604 AATGCACTGTGTGATCGAATGATATAGGAAAGGCGCCGACATGATCCAGTATGTTG 663
 Db 258 AsnAlaProValTrpIleGluTrpTyrArgLysArgProAspMetAsnProValValLeu 277
 QY 664 GAGCTTGCCTACTCGCTTAAATTTCTCAAGCACAAATTTCAAGAGAGCTCAAGAA 723
 Db 278 GluLeuAlaIleLeuAspLeuAsnIleValGlnAlaGlnPheGlnGluLeuLysGlu 297
 QY 724 TCCTTCAGGTGGTGGAGAAATCTAGGTTTCTGAGAGCTGCCCTTCGCAAGGATAGA 783
 Db 298 SerPheArgTrpTrpArgAsnThrGlyPheValGluLysLeuProPheAlaArgAspArg 317

QY 784 CTGGTGAATGCTACTTTTGGAAATCTGGGATCATCGAGCCAGCTCAGCATGCAAGTGA 843
 Db 318 LeuValGluCysTyrPheTrpAsnThrGlyIleIleGluProArgGlnHisAlaSerAla 337
 QY 844 AGGATAATGATGGCAAAAGTCAACCTCTGATTACGGTGATCGATCATATTTATGATGC 903
 Db 338 ArgIleMetMetGlyLysValAsnAlaLeuIleThrValIleAspAspIleTyrAspVal 357
 QY 904 TATGGCACCTTTAGAAGAACTCGAACAAATTCACCTGACCTCATTCGAAGATGGGATATAAC 963
 Db 358 TyrGlyThrLeuGluGluLeuGlnPheThrAspLeuIleArgArgTrpAspIleAsn 377
 QY 964 TCAATCGACCAACTTCCGATTACATGCAACTGCTCTTCTTGCACCTCAACACTTCGC 1023
 Db 378 SerIleAspGlnLeuProAspTyrMetGlnLeuCysPheLeuAlaLeuAsnAsnPheVal 397
 QY 1024 GATGATACATCGTACGATGTTTATGAAGGAGAAAGCGCTCAACGTTTATACCTACCTCGCG 1083
 Db 398 AspAspThrSerTyrAspValMetLysGluLysGlyValAsnValIleProTyrLeuArg 417
 QY 1084 CAATCGTGGTGTGATTGGCGGATAGTATATAGTAGAGGACGGTGGTCTACGGCGG 1143
 Db 418 GlnSerTrpValAspLeuAlaAspLysTyrMetValGluAlaArgTrpPheTyrGlyGly 437
 QY 1144 CACAAACCAAGTTTGAAGAGTATTGGAGAACTCATGGCAGTCGATAAGTGGGCCCTGT 1203
 Db 438 HisLysProSerLeuGluGluTyrLeuGluAsnSerTrpGlnSerIleSerGlyProCys 457
 QY 1204 ATGTTAACCCACATATCTTCGAGTAACAGATTCGTTCCAAAGAGACCGTCGACAGT 1263
 Db 458 MetLeuThrHisIlePhePheArgValThrAspSerPheThrLysGluThrValAspSer 477
 QY 1264 TTGTCAAAATACCAAGTATTGTTGCTTCATCTCTGCTGCTGCGGCTTGTGATGAT 1323
 Db 478 LeuTyrLysTyrHisAspLeuValArgTrpSerSerPheValLeuArgLeuAlaAspAsp 497
 QY 1324 TTGGGAACCTCGTGGAGAGTGACAGAGGGATGTCCGAAATCATCTCAGTCTAC 1383
 Db 498 LeuGlyThrSerValGluGluValSerArgGlyAspValProLysSerLeuGlnCysTyr 517
 QY 1384 ATGAGTGAATCAATGATCGATCGAGCGGAGCGGAGCGGAGCGGAGCGGAGCGGAGCG 1443
 Db 518 MetSerAspTyrAsnAlaSerGluAlaGluAla-glyHisValLysTrpLeuIleAla 537
 QY 1444 GAGGTGTGAAGAAAGTGAATCGGAGAGGGTGTGGAAGGATTCCTCATTCGCGCAAAGAT 1503
 Db 538 GluValTrpLysLysMetAsnAlaGluA-gValSerLysAspSerProPheGlyLysAsp 557
 QY 1504 TTTATAGGATGTGCGAGTTGATTAGGAAGATGGCGCAGTTGATGATCATTAATGAGAT 1563
 Db 558 PheIleGlyCysAlaValAspLeuGlyArgMetAlaGlnLeuMetTyrHisAsnGlyAsp 577
 QY 1564 GGSCACGCGACACACACCTTATTATACATCAACAAATGACAGAACCTTATTTCGAGCC 1623
 Db 578 GlyHisGlyThrGlnHisProIleIleHisGlnGlnMetThrArgThrLeuPheGluPro 597
 QY 1624 TTGCA 1629
 Db 598 PheAla 599

RESULT 5
 ; Sequence 24, Application US/09887586A
 ; Patent No. US20020094556A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chappell, Joseph
 ; APPLICANT: No. US20020094556A1, Joseph P.
 ; APPLICANT: Starks, Courtney M.
 ; APPLICANT: Manna, Kathleen R.
 ; TITLE OF INVENTION: SYNTHASES
 ; FILE REFERENCE: 07678-025001
 ; CURRENT APPLICATION NUMBER: US/09/887,586A

```

; CURRENT FILING DATE: 2001-06-22
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 24
; TYPE: PRT
; ORGANISM: Salvia officinalis
; US-09-887-586A-24

Alignment Scores:
Pred. No.: 1,116-143 Length: 591
Score: 1633.50 Matches: 305
Percent Similarity: 75.96% Conservative: 109
Best Local Similarity: 55.96% Mismatches: 116
Query Match: 56.17% Indels: 15
DB: 9 Gaps: 7

US-09-938-956-6 (1-1632) x US-09-887-586A-24 (1-591)

QY 4 AGAGCATCCGGAACATACACCTTCCTCGTTGGATGTCAACTTCATCCAAATCGCTTCTC 63
Db 57 ArgArgThrGlyGlyTyrGlnProThrLeuTyrAspPheSerThrIleGlnLeuPheAsp 76
QY 64 AGTGAATTAAGAGACACACGTTGATTCGGCTTCCTGAGCTGGTCACTTGTGTGAAG 123
Db 77 SerGluTyrLysGlnGluLysHisLeuMetArgAlaAlaGlyMetIleAlaGlnValAsn 96
QY 124 ATCGCACTGAGAAAGAAAGCGATCAATTCGACAACTTGAGTGTGATCGATCGACTTGCAG 183
Db 97 MetLeuLeuGlnGluValAspSerIleGlnArgLeuGluLeuIleAspLeuArg 116
QY 184 AGATGGGGTCTCGCATCATTTCCAAATGAGTCCAAAGATCTTGCCTCTATATAT 243
Db 117 ArgLeuGlyIleSerCysHisPheAspArgGluIleValGluLeuAsnSerLysTyr 136
QY 244 CTCGACCATCACTATTACAGAACCTTTTCCAAAGAAAGAGGATCTCTACTCCACA 303
Db 137 -----TyrThrAsnAsnGluIle-----AspGluSerAspLeuTyrSerThr 150
QY 304 TCTCTTGCACTTATAGGCTCTCAGAGAACATGTTTCAAGTCGCAACAGAGTATTCGAT 363
Db 151 AlaLeuArgPheLysLeuLeuArgGlnTyrAspPheSerValSerGlnGluValPheAsp 170
QY 364 AGTTTCAGAACAGAGGGGT---GAGTTCAAAGAAAGCCTTAGCGACGACACCCAGGA 420
Db 171 CysPheLysAsnAspLysGlyThrAspPheLysProSerLeuValAspAspThrArgGly 190
QY 421 TTGTTGCACTGATGAGCTTCTCTTCTGTCGCGAAGCGGAAACACCGCTCGAGTCA 480
Db 191 LeuLeuGlnLeuTyrGluAlaSerPheLeuSerAlaGlnGlyGluGluThrLeuHisLeu 210
QY 481 GCGAGGAATTCGCCACCAATTTTGGAGGAAAAAGTGNACGAGGGTGGTGTGATGGC 540
Db 211 AlaArgAspPheAlaThrLysPheLeuHisLysArgValLeu-----ValAspLys 227
QY 541 GAC-----CTTTTAAACAAGATCGCATATTCCTTGGACATCCCTCTTCATTGGAGGAT 594
Db 228 AspIleAsnLeuLeuSerSerIleGluArgAlaLeuGluLeuProThrHisTyrArgVal 247
QY 595 AAAAGGCCAAATGCACTGTGTGATCGAATGATGTATAGGAGGCGCGACATGATCCA 654
Db 248 GlnMetProAsnAlaArgSerPheIleAspAlaTyrLysArgArgProAspMetAsnPro 267
QY 655 GTAGTGTGTGAGCTTGCATACCTGAGCTTAAATATTGTTCAACACAAATTTCAAGAGAG 714
Db 268 ThrValLeuGluLeuAlaLysLeuAspPheAsnMetValGlnAlaGlnPheGlnGlnGlu 287

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715 CTCAAAGAATCCCTTCAGGTGGTGGAGAAATACCTGGTGTGTTGTTGAGAAGCTCCCTTCGCA 774
288 LeuLysGluAlaSerArgTyrPheAsnSerThrGlyLeuValHisGluLeuProPheVal 307
775 AGGATAGACTGGTGGATCTACTTTTGGAAATCTGGGATCATCGAGCCACCTCAGCAT 834
308 ArgAspArgIleValGluCysTyrTyrTrpThrThrGlyValValGluArgArgGluHis 327
835 GCAAGTCAGGATTAATGATGGGCAAGTCAACGCTCTGATTACGGTGTGATCGATGATATT 894
328 GlyTyrGluArgIleMetLeuThrLysIleAsnAlaLeuValThrThrIleAspAspVal 347
895 TATGATCTTATGCGACCTTTAGAAACCTCGAAATTCATCTGACCTCATTCGAAAGATGG 954
348 PheAspIleTyrGlyThrLeuGluGluLeuGluLeuPheThrThrAlaIleGlnArgTyr 367
955 GATATAAACTCAATCGACCACTCCCGATTACATCACTGCTGCTTTCTTTCACCTCAAC 1014
368 AspIleGluSerMetLysGlnLeuProTyrMetGlnIleCysTyrLeuAlaLeuPhe 387
1015 AACTTCGTCGATGATACATCGTACGATGTTTATGAAGAGAGAAAGCGCTCAACGTTATACC 1074
388 AsnPheValAsnGluMetAlaTyrAspThrLeuArgAspLysGlyPheAsnSerThrPro 407
1075 TACTTCGGCAATCGTGGTGTGTTGTCGGGATAAGTATATGTTAGAGGACCGTGTTC 1134
408 TyrLeuArgLysAlaTyrValAspLeuValGluSerTyrLeuIleGluAlaLysTyrTyr 427
1135 TACGCGCGGACAAACCAAGTTTGGAAAGATATTGGAAGAACTCATCGCAGTCCGATAGT 1194
428 TyrMetGlyHisLysProSerLeuGluGluTyrMetLysAsnSerTyrIleSerIleGly 447
1195 GGGCCCTGTATGTTAAACGACATATTCCTCGAGTAAACAGATTCGTTCAACAGGAGACC 1254
448 GlyIleProIleLeuSerHisLeuPhePheArgLeuThrAspSerIleGluGluGluAsp 467
1255 GTCCACAGTTTGTACAAATACCAAGTATTAGTTCTGTTGTCATCTCTTCGTCGGCTT 1314
468 AlaGluSerMetHisLysTyrHisAspIleValArgAlaSerCysThrIleLeuArgLeu 487
1315 GCTGATGATTTGGAACTCCTCGTGGAAAGAGTGAAGAGAGGAGATGTCGCGAATCATCTT 1374
488 AlaAspAspMetGlyThrSerLeuAspGluValGluArgGlyAspValProLysSerVal 507
1375 CAGTCTACATGATGACTACATCGATCGAGGCGGAGCGGAGCGGAGCGGAGCGGAGCGG 1434
508 GlnCysTyrMetAsnGluLysAsnAlaSerGluGluAlaArgGluHisValArgSer 527
1435 CTGATAGCGGAGGTGTGGAAGAGATGAATCGGAGAGGGGTGTGGAAGGATTCCTCATTC 1494
528 LeuIleAspGlnThrTyrLysMetMetAsnLysGluMetMetThr-----SerSerPhe 545
1495 GCGAAAGATTTTATAGATGTCAGTGTGATTTAGGAGGATGCGGAGGATGATGATGATC 1551
546 SerLysTyrPheValGlnValSerAlaAsnLeuAlaArgMetAlaGlnTyrIleTyrGln 565
1552 CATATGAGATGGGCGGACGACACCAACACCTTATTATACATCAACAAATGACCGAGAAC 1611
566 HisGluSerAspGlyPheGlyMetGlnHisSerLeuValAsnLysMetLeuArgGlyLeu 585
1612 TTATTCGAGCCCTTT 1626
586 LeuPheAspArgTyr 590

RESULT 6
US-09-903-012-24
; Sequence 24, Application US/09903012
; Patent No. US20020094557A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094557A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.

```

; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Salvia officinalis
US-09-903-012-24
Alignment Scores:
Pred. No.: 1,11e-143 Length: 591
Score: 1633.50 Matches: 305
Percent Similarity: 75.96% Conservative: 109
Best Local Similarity: 55.96% Mismatches: 116
Query Match: 56.17% Indels: 15
DB: 9 Gaps: 7
US-09-938-956-6 (1-1632) x US-09-903-012-24 (1-591)
QY 4 AGAGCATCCGAAACTACAACTCCGTTGGGATGTCACATTCATCCAACTGCTCTC 63
DB 57 ArgarginGlyGlyTyGlnProthrLeuTrpAspPheSerThrIleGlnLeuPheAsp 76
QY 64 AGTGACTATAAGGAGGACAAACACGTGATTAGGCTTCTGAGCTGGTGCATTTGGTGAAG 123
DB 77 SerGluTyLysGluGluLysHisLeuMetArgAlaAlaGlyMetIleAlaGlnValAsn 96
QY 124 ATGGAATCGAGAAAGAACCGATCAATTCGACACCTTGAGTTCGATGATCGATTCGAG 183
DB 97 MetLeuLeuGlnGluGluValAspSerIleGlnArgLeuGluLeuIleAspAspLeuArg 116
QY 184 AGGATGGGGCTGTCGGATCAATTCGAAATAGTTCGAAAGAAATCTTGCTCTATATAT 243
DB 117 ArgLeuGlyIleSerCysHisPheAspArgGluIleValGluIleLeuAsnSerLysTy 136
QY 244 CTCGACCATCTATTACAAACCCCTTTCCAAAGAGAAAGAGGATCTCTACTCCACA 303
DB 137 -----TyThrAsnAsnGluIle-----AspGluSerAspLeuTySerThr 150
QY 304 TCTCTTGCACTTAGGCTCCTCAGAACATCGTTTCAAGTCGACACAGAGGTATTCGAT 363
DB 151 AlaLeuArgPheLysLeuLeuArgGlnTyRAspPheSerValSerGlnGluValPheAsp 170
QY 364 AGTTTCAGAACGAGGAGGT---GAGTTCAGAAAGCCCTTAGCGACGACACGAGGA 420
DB 171 CysPheLysAsnAspLysGlyThrAspPheLysProSerLeuValAspAspThrArgGly 190
QY 421 TTGTTGCACTGTATGAGCTTCCTTCTGTTGACGAGGAGGAAACGACCTCGAGTCA 480
DB 191 LeuLeuGlnLeuTyGlnAlaSerPheLeuSerAlaGlnGlyGluGluThrLeuHisLeu 210
QY 481 GCGAGGAATCCGCCACCAAAATTTTGGAGGAAAGTGAACGAGGGTGTGTGTGATGCG 540
DB 211 AlaArgAspPheAlaThrLysPheLeuHisLysArgValLeu-----ValAspLys 227
QY 541 GAC-----CTTTAAACAGAAATCCATATCTTTGGACATCCCTCTTCATGGAGATT 594
DB 228 AspIleAsnLeuLeuSerSerIleGluArgAlaLeuGluLeuProThrHisIleTrpArgVal 247
QY 595 AAAAGGCCAAATGCACCTGTGTGGATCGAATGGTATAGAGAGGCCCGACATCAATCCA 654
DB 248 GlnMetProAsnAlaArgSerPheIleAspAlaTyLysArgArgProAspMetAsnPro 267

RESULT 7

US-09-900-797-24
; Sequence 24, Application US/09900797
; Publication No. US20030087406A1

QY 655 GTAGTGTGGAGCTTGGCATACTCGACTTAAATATTGTTCAAGCACAATTTCAAGAGAG 714
DB 268 ThrValLeuGluLeuAlaLysLeuAspPheAsnMetValGlnAlaGlnPheGlnGlnGlu 287
QY 715 CTCAAAGATCCTTCAGGTGGTGGAAATACTGGTTTGTGAGAAGCTGCCCTTCGCA 774
DB 288 LeuLysGluAlaSerArgTrpAsnSerThrGlyLeuValHisGluLeuProIleVal 307
QY 775 AGGGATAGACTGCTGGAATCTACTTTTGGAACTATCGGATCATCGAGCCAGTCAGCAT 834
DB 308 ArgAspArgIleValGluCysTyTrpThrThrGlyValValGluArgGluHis 327
QY 835 GCAAGTGCAGGATTAATGATGGGAAAGCAAGCTCTGATTCAGTGTACGATCATATATT 894
DB 328 GlyTyGluArgIleMetLeuThrLysIleAsnAlaLeuValThrThrIleAspVal 347
QY 895 TATGATGCTCTATGTCACCTTACAGAACTTCGAACAATTCACCTGACCTCATTCGAAAGATGG 954
DB 348 PheAspIleTyGlyThrLeuGluLeuGlnLeuPheThrThrAlaIleGlnArgTrp 367
QY 955 GATATAAACTCAATCGACCAACTTCCGATTAACATGCAACTGTGTCTTCTTCATCACTCAAC 1014
DB 368 AspIleGluSerMetLysGlnLeuProTyMetGlnIleCysTyLeuAlaLeuPhe 387
QY 1015 AACTTCGTGATGATACATCGTACGATGTTATGAAGGAGAGAGGCTCAACGTTATACCC 1074
DB 388 AsnPheValAsnGluMetAlaTyRAspThrLeuArgAspLysGlyPheAsnSerThrPro 407
QY 1075 TACCTCGCGCAATCGTGGTTCATTGGCGGATAAGTATATCGTAGAGCACAAGTGTTC 1134
DB 408 TyRLeuArgLysAlaTrpValAspLeuValGluSerTyRLeuIleGluAlaLysTrpTy 427
QY 1135 TACGGCGGCAACCAACCAAGTTTGGAGAGTATTTGGAGAACTCATGTCAGTCGATAAGT 1194
DB 428 TyRMetGlyHisLysProSerLeuGluTyRMetLysAsnSerTrpIleSerIleGly 447
QY 1195 GGGCCCTGATGTTAAGCAGCACAATTTCTTCCAGATAACAGATTCGTTTCAAGAGAGACC 1254
DB 448 GlyIleProIleLeuSerHisLeuPheArgLeuThrAspSerIleGluGluAsp 467
QY 1255 GTCGACAGTTTGTACAAATACACAGATTAGTTCGTTGCTTCATCTCTGCTTCGCGCTT 1314
DB 468 AlaGluSerMetHisLysTyRHisAspIleValArgAlaSerCysThrIleLeuArgLeu 487
QY 1315 GCTGATGATTGGGAACCTCGGTGGAAGAGGTGAGCAGAGGGGATGTCGCGAAATCACTT 1374
DB 488 AlaAspAspMetGlyThrSerLeuAspGluValGluArgGlyAspValProLysSerVal 507
QY 1375 CAGTCTACATGATGATCAATCATCGAGGCGGAGCGGAGCGGAGCAGTGAATGG 1434
DB 508 GlnCysTyRMetAsnGluLysAsnAlaSerGluGluGluAlaArgGluHisValArgSer 527
QY 1435 CTGATAGCGGAGGTGTGGAAGAGATGATCGGAGAGGCTGTCGAAGGATTCCTCATTC 1494
DB 528 LeuIleAspGlnThrTrpLysMetMetAsnLysGluMetMetThr-----SerSerPhe 545
QY 1495 GGCAGAGATTTTATAGGATGTCGATGTTGATTTAGGAAGGATGCGCAGTTGATGTAC--- 1551
DB 546 SerLysTyRValGlnValSerAlaAsnLeuAlaArgMetAlaGlnTrpIleTyRVal 565
QY 1552 CATATGGAGATGGGACCGCACACACCTTATATACATCAACAATGACCAGAAC 1611
DB 566 HisGluSerAspGlyPheGlyMetGlnHisSerLeuValAsnLysMetLeuArgGlyLeu 585
QY 1612 TTATTCGAGCCCTTT 1626
DB 586 LeuPheAspArgTyR 590

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; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US2003087406A11, Joseph P.
; APPLICANT: Starke, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/900,797
; CURRENT FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US/09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; TYPE: PRT
; LENGTH: 591
; ORGANISM: Salvia officinalis
; US-09-900-797-24

Alignment Scores:
Pred. No.: 1,116-143 Length: 591
Score: 1633.50 Matches: 305
Percent Similarity: 75.96% Conservative: 109
Best Local Similarity: 55.96% Mismatches: 116
Query Match: 56.17% Indels: 15
DB: 10 Gaps: 7

US-09-938-956-6 (1-1632) x US-09-900-797-24 (1-591)

QY 4 AGACGATCCGGAACATACACCCCTTCCTGGTGGATGTCACATTCATCCAAATCGCTTCTC 63
Bb 57 ArgArgThrGlyGlyTyrGlnProThrLeuTyrAspPheSerThrIleGlnLeuPheAsp 76
QY 64 AGTGACTATAAGGAGACACACGATGATAGGCTTCGACGTTCGACCTTCGTCAGG 123
Db 77 SerGluTyrLysGluGluLysHisLeuMetArgAlaAlaGlyMetIleAlaGlnValAsn 96
QY 124 ATCGAACTGGAGAAAGACGATCAATTCGACAACTTGATGATCGATCGACTTGCAG 183
Db 97 MetLeuLeuGlnGluGluValAspSerIleGlnArgLeuGluLeuIleAspLeuArg 116
QY 184 AGGATGGGTGTCGATCATTTCCAAATGAGTTCAAAGAAATCTTGCTCTATATAT 243
Db 117 ArgLeuGlyIleSerCysHisPheAspArgGluIleValGluLeuAsnSerLysTyr 136
QY 244 CTCGACCATCACATATTACAGAACCCCTTTCCAAAGAAAGAGGATCTCTACTCCACA 303
Db 137 -----TyrThrAsnAsnGluIle-----AspGluSerAspLeuTyrSerThr 150
QY 304 TCTCTTGCAATTAAGTCTCAGAGAACATGTTTCAAGTCCGACACAGAGTATTCGAT 363
Db 151 AlaLeuArgPheLysLeuLeuArgGlnTyrAspPheSerValSerGlnGluValPheAsp 170
QY 364 AGTTTCAAGAACAGAGGGGT---GAGTTCAAGAAAGCTTAGCGACACACACAGAGA 420
Db 171 CypPheLysAsnAspLysGlyThrAspPheLysProSerLeuValAspAspThrArgGly 190
QY 421 TTGTTCGAATGTATGAAGTCTCTTCTGTCGACGAGGCGGAAACCCACGTCGAGTCA 480
Db 191 LeuLeuGlnLeuTyrGluAlaSerPheLeuSerAlaGlnGlyGluGluThrLeuHisLeu 210
QY 481 GCGAGGAATCCGCCACCAATTTTGGAGAAAAGTGAACGAGGGTGGTTCGATGCG 540
Db 211 AlaArgAspPheAlaThrLysPheLeuHisLysArgValLeu-----ValAspLys 227
QY 541 GAC-----CTTTTAAACAAGATCGCATATCTTTGGACATCCCTTCTCATTGGAGGAT 594
Db 228 AspIleAsnLeuLeuSerSerIleGluArgAlaLeuGluLeuProThrHisIleArgVal 247

595 AAAAGGCCAAATCACCTGTGTGGATCGAATGATAGGAAGAGGCCCGACATGAATCCA 654
248 GlnMetProAsnAlaArgSerPheIleAspAlaTyrLysArgArgProAspMetAsnPro 267
655 GTAGTGTGGAGTTCGCATACCTGCTAAATATTGTTCAAGACACAAATTTCAAGAGAG 714
268 ThrValLeuGluLeuAlaLysLeuAspPheAsnMetValGlnAlaGlnPheGlnGlu 287
715 CTCAAAGAATCCTTCAGGTGGTGGAGAAATACCTGGGTTTGTTCGAGAAGCTGCCCTCGCA 774
288 LeuLysGluAlaSerArgIlePheAsnSerThrGlyLeuValHisGluLeuProPheVal 307
775 AGGATAGACTGGTGAATCTACTTTTGGAAATCTGGGATCATCGAGCCACCTCAGCAT 834
308 ArgAspArgIleValGluCysTyrTyrThrThrGlyValValGluArgGluHis 327
835 GCAAGTCARAGGATATGATGGGCAAGTCAACGCTCTGATTAACGCTGATCGATGATATT 894
328 GlyTyrGluArgIleMetLeuThrLysIleAsnAlaLeuValThrIleAspAspVal 347
895 TATGATGCTTATGCGACCTTAGAAGAACCTCAATTCATCTCAGCTCATTCGAAAGATGG 954
348 PheAspIleTyrGlyThrLeuGluGluLeuPheThrThrAlaIleGlnArgTyr 367
955 GATATAAATCAATCGACCACTTCGCGATATAGTCACTGCTGCTTCTTCTGCACTCAAC 1014
368 AspIleGluSerMetLysGlnLeuProTyrMetGlnIleCysTyrLeuAlaLeuPhe 387
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388 AsnPheValAsnGluMetAlaTyrAspThrLeuArgAspLysGlyPheAsnSerThrPro 407
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408 TyrLeuArgLysAlaTyrValAspLeuValGluSerTyrLeuIleGluAlaLysTyrTyr 427
1135 TACGCGCGGACACAAACCAAGTTTGGAGAGTATTGAGAACTCATCGTCACTGATGAAGT 1194
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448 GlyIleProIleLeuSerHisLeuPhePheArgLeuThrAspSerIleGluGluAsp 467
1255 GTCGACAGTGTGACAAATACACGATTTAGTTGCTGTTGTCATCTCTGTTCTGCGCTT 1314
468 AlaGluSerMetHisLysTyrHisAspIleValArgAlaSerCysThrIleLeuArgLeu 487
1315 GCTGATGATTTGGAACTCGTGGAGAGAGTGCAGAGAGAGGATGTCGCGAATCACTT 1374
488 AlaAspAspMetGlyThrSerLeuAspGluValGluArgGlyAspValProLysSerVal 507
1375 CAGTGTACATGAGTACTACATGCTCGAGCGGAGCGGCGGAGGAGCGTGAATGG 1434
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1435 CTGATAGCGAGGTGTGGAAAGATGAATCGCGAGAGGGGTGTCGAAGGATTCCTCATTC 1494
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1495 GCGAAAGATTTATAGATGTCGATGTCAGTTAGGAGGATGGCGAGTTCATGATGAC--- 1551
546 SerLysTyrPheValGlnValSerAlaAsnLeuAlaArgMetAlaGlnTyrIleTyrGln 565
1552 CATTAATGAGATGGGACGCGCACACACCCCTTATATATACATCAACAAATGACCGAGACC 1611
566 HisGluSerAspGlyPheGlyMetGlnHisSerLeuValAsnLysMetLeuArgGlyLeu 585
1612 TTATTCGAGCCCTTT 1626
586 LeuPheAspArgTyr 590
RESULT 8
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[illegible]

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Db      585 LeuPheGlnProTyr 589
RESULT 9
US-09-903-012-54
; Sequence 54, Application US/09903012
; Patent No. US20020094557A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094557A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 590
; TYPE: PRF
; ORGANISM: Salvia officinalis
US-09-903-012-54

Alignment Scores:
Pred. No.:      3,43e-136      Length:      590
Score:          1553.50        Matches:    291
Percent Similarity: 72.48%      Conservative: 104
Best Local Similarity: 53.39%    Mismatches: 141
Query Match:     53.42%         Indels:     9
DB:              9             Gaps:       3

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Db      51 IleArgArgSerGlyAspTyrGlnProSerLeuTyrPheAsnTyrIleGlnSerLeu 70
QY      61 CTGAGTACTATAAGAGAGACAAACACGTGATTAGGGCTTCGAGCTGCTCACTTTGGTG 120
Db      71 AsnThrProTyrIleGlnArgHisPheAsnA-gGlnAlaGluLeuIleMetGlnVal 90
QY      121 AGATCGAACTGAGAGAAAGAAAGGATCAAAATTCGACAACTTGATGATCGATGCTTG 180
Db      91 ArgMetLeuLeuLysValLysMetGluAlaIleGlnGlnLeuGluLeuIleAspLeu 110
QY      181 CAGAGATGGGGCTGCCGATCATTTCCAAATAGTTCAAAGAAATCTTGCTCTATA 240
Db      111 GlnTyrLeuGlyLeuSerTyrPheGlnAspGluIleGlnLeuSerSerile 130
QY      241 TATCTCGACCATCATTTATCAAGAACCCCTTTTCCAAAGAGAAAGGATCTTACTCC 300
Db      131 HisAsnGluProArgTyrPheHisAsn-----AsnAspLeuTyrPhe 144
QY      301 ACCTCTTCATTAGTCTCCTCAGAGACATGTTTCAAGTCGACAGAGATTC 360
Db      145 ThrAlaLeuGlyPheArgIleLeuArgGlnHisGlyPheAsnValSerGluAspValPhe 164
QY      361 GATAGTTTCAAGAACGAGAG---GGTGAATTCAAGAAAGGCTTAGCGACGACACCGAGA 417
Db      165 AspCysPheLysIleGluLysCysSerAspPheAsnAlaAsnLeuAlaGlnAspThrLys 184
QY      418 GGATTTCTCACTGATGATGCTCTTCTGTCGACGAGGCGAAACCGACGCTCGAG 477
Db      185 GlyMetLeuGlnLeuTyrGluAlaSerPheLeuLeuArgGluGlyGluAspThrLeuGlu 204

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185	GlyMetLeuGlnLeuTyrgluAlaSerPheLeuLeuArgGluGlyGluAspThrLeuGlu	204
478	TCAGCGAGGGAATCCGACCAAAATTTTGGAGGAAAAAGTCAACAGAGGCTGTG	531
205	LeuAlaArgArgPheSerThrArgSerLeuArgGluLysPheAspGluGlyAspGlu	224
532	GTTGATGGCGACTTTTAAACAAGATCGCATATTCTTTGGACATCCCTCTTCATCGGAGG	591
225	IleAspGluAspLeuSerSerTrpIleArgHisSerLeuAspLeuProLeuHisTrpArg	244
592	ATTAAAGGCCAAATGACCTCTGTGTGATCGAATGTATAGGAAGAGGCCGACATGAAT	651
245	ValGlnGlyLeuGluAlaArgTrpPheLeuAspAlaTyAlaArgArgProAspMetAsn	264
652	CCAGTAGTGTGGAGCTTCCCATACTCGACTTAATAATTATTGTTCAAGCACAAATTTCAAGAA	711
265	ProLeuIlePheLysLeuAlaLysLeuAsnPheAsnIleValGlnAlaThrTyrglnGlu	284
712	GAGCTCAAGAATCCCTTCAGGTGGTGAGAAATACTGGGTTTCTTGAGAAGCTGCCCTTC	771
285	GluLeuLysAspIleSerArgTrpTrpAsnSerSerCysLeuAlaGluLysLeuProPhe	304
772	GCAAGGATAGACTGGTGGAAATGCTACTTTTGGAAATCTGGGATCATCGAGCGACAGTCAG	831
305	ValArgAspArgIleValGluCysPhePheTrpAlaIleAlaPheGluProHisGln	324
832	CATGCAAGTGCAGGATATGATGGCAAGTCAACGCTCTGTATTACGGTGATCGATGAT	891
325	TyrSerTyrgluArgLysMetAlaAlaValIleIleThrPheIleThrIleIleAspAsp	344
892	ATTATTGATGCTCATGGCACCTTAGAAGAAGCTCGAAACAATCTACTGACCTCATCTCGAAGA	951
345	ValTyArgValTyrglyThrIleGluGluLeuGluLeuLeuThrAspMetIleArgArg	364
952	TGGGATATAAATCAATCACCACCACTCCGATTACATGCAACTGTGCTTTCTTGCACTC	1011
365	TrpAspAsnLysSerIleSerGlnLeuProTyTyMetGlnValCysTyrgluAlaLeu	384
1012	AACAACTTCGTGCATCATCATCGTACGATGTTATGAAGAGAGAAAGCGCTCAACGTTATA	1071
385	TyrAsnPheValSerGluArgAlaTyArgPheIleLeuLysAspGlnHisPheAsnSerIle	404
1072	CCTACTCGGGCAATCGTGGTGTGATTTGCGCGATAAGTATATGTTAGGAGGCAGCTGG	1131
405	ProTyrgluGlnArgSerTrpValSerLeuValGluGlyTyrgluLysGluAlaTyArg	424
1132	TTCTACGGGGGCACAAACCAAGTTTGGAGAGTATTTGAGAACTCATGCGCATCGGATA	1191
425	TyTyArgGlyTyrgLysProSerLeuGluGluTyrgLeuAsnAsnAlaLysIleSerIle	444
1192	AGTGGCCCTGTATGTTAAACGACATATTTCTCCGAGTAAACAGATTCTGTTCAACAAGAG	1251
445	SerAlaProThrIleIleSerGlnLeuTyPheThrLeuAlaAsnSerIleAspGluThr	464
1252	ACCGTCGACAGTTGTGACAAATACCAAGATTAGTTCGTTTGGTTCATCTCTGTTCTCGCG	1311
465	AlaIleGlnSerLeuTyrgLinyrHisAsnIleLeuTyrgLeuSerGlyThrIleLeuArg	484
1312	CTTGCTGATGANTTGGGAACCTCGGTGGAAGAGGTGACAGAGGGGATGTGCCGAATCA	1371
485	LeuAlaAspAspLeuGlyThrSerGlnHisGluLeuGluArgGlyAspValProLysAla	504
1372	CTTCAGTGTACATGATGACTACATGCAATCGAGCGGAGCGCGGAGACAGTGAAGAA	1431
505	IleGlnCysTyrgMetAsnAspThrAsnAlaSerGluArgGluAlaValGluHisValLys	524
1432	TGCGCTATACGGAGGTGTGGAAGAAGATGAATGCGGAGAGGGTGTGCGAAGGATCTCCCA	1491
525	PheLeuIleArgGluAlaTrpLysGluMetAsnThrValThrThrAlaSerAspCysPro	544
1492	TTCGGCAAGATTTTATGAGATGTGCAGTTGATTTAGGAAGGATGGCGCAGTTGATGAC	1551

Ddb		S56	LeuAspGlyAepGlyHieGlyValGlnHisSerGlurIleSclnMetdGlyLeu	584
QY		1612	TTATTCGAGCCCTTT	1626
Ddb		585	LeuPheGlnProTyr	589
 RESULT 10 US-09-900-797-54 ; Sequence 54, Application US/09900797 ; Publication No. US20030087406A1 ; GENERAL INFORMATION: ; APPLICANT: Chappell, Joseph ; APPLICANT: NO. US20030087406A1, Joseph P. ; APPLICANT: Starks, Courtney M. ; APPLICANT: Mauna, Kathleen R. ; TITLE OF INVENTION: SYNTHASES ; FILE REFERENCE: 07678-025001 ; CURRENT APPLICATION NUMBER: US/09/900,797 ; CURRENT FILING DATE: 2001-07-06 ; PRIOR APPLICATION NUMBER: US/09/398,395 ; PRIOR FILING DATE: 1999-09-17 ; PRIOR APPLICATION NUMBER: 60/130,628 ; PRIOR FILING DATE: 1999-04-22 ; PRIOR APPLICATION NUMBER: 60/150,262 ; PRIOR FILING DATE: 1999-08-23 ; NUMBER OF SEQ ID NOS: 58 ; SOFTWARE: FastSeq for Windows Version 3.0 ; SEQ ID NO 54 ; LENGTH: 590 ; TYPE: PRN ; ORGANISM: Salvia officinalis US-09-900-797-54 Alignment Scores: Prld. No.: 3.43e-136 Length: 590 Score: 1553.50 Matches: 291 Percent Similarity: 72.48% Conservative: 104 Best Local Similarity: 53.39% Mismatchches: 141 Query Match: Indels: 9 DB: Gaps: 3 US-09-938-956-6 (1-1632) x US-09-900-797-54 (1-590) QY 1 ATGACACCATCGGAACACTCAACCCCTCTGTGGGATGTCAACTTCATCCAATCGCCTT 60 Ddb ::: ::: ::: ::: ::: ::: ::: 51 lleARgSRerGlyASPTy-GlnProSerLeuTrlpaspPheasnTyrlleGlnSerLeu 70 QY 61 CTCAGTGACTATAAGGAGCACAAAACAAGTATTAGGCCTTCTGAGCTGTGCTACTTTGGTG 120 Ddb ::: ::: ::: ::: ::: ::: ::: 71 AsnThrProTyrLysGluInArgHisPheAsnArgGlnAlaGluLeuIleMetGlnVal 90 QY 121 AAGATGGGAATCGGAGAAGAACCGATCAAATTCGACAACTTCAGTTTGATCGATGACTTG 180 Ddb ::: ::: ::: ::: ::: ::: ::: 91 ArgMetLeuLeuLysValLysMetGluAlaIlegInlneudGluLeuleasplapLeu 110 QY 181 CAGAGGATGGGGCTCTCGATCATTTCCAAATAGATTCAAAGAAATFTTGCTCTATA 240 Ddb ::: ::: ::: ::: ::: ::: ::: 111 GlnTyrLeuGlyLeuSer-Tyr-PhePheGlnAspGluileLysGlnileLeuSerSerIle 130 QY 241 TATCTCGACCATCATTATACAAGACCCCTTTCCAAAAGAGGAAGGATCTCTACTCC 300 Ddb ::: ::: ::: ::: ::: ::: ::: 131 HisAsnGluProArgTyr-PheHisAsn-----AenAspLeuTyrPhe 144 QY 301 ACATCTCTTGCAATTTTAGCTCTCTCAGAGAAATGGTTTTCAAGTCGCGACAAGAGGTATTTC 360 Ddb ::: ::: ::: ::: ::: ::: ::: 145 ThrAlaLeuGlyPheArgIleleuArgGlnHisGlyPheAsnValSerGluAspValPhe 164 QY 361 GATAGTTTCAAGAACGAGAG---GGTGAGTTCAAAGAGCCCTTAGCGACGACACAGA 417 Ddb :: : :: : :: : :: : :: : :: : 165 AspCysPheLysIleGluLysCysSerASPpheAsnAlaAsnLeuAlaGlnAspThrLys 184 QY 418 GCATGTTGTCRAACTGTATGAGCTTCCTTTCTGTGGAGGAGCGCAAAACGAGCTCGAG 477 Ddb :: : :: : :: : :: : :: : :: :				

173 AsnCysPheLysAsnGluLysGlyIleAspPheLysAlaSerLeuAlaGlnAspThrLys 192

418 GGATGTTGCAACGTGTAAGAAGCTTCCTTCTGTTGACGGAAGCGGAACACACCTCGAG 477

193 GlyMetLeuGlnLeuTyrrGluAlaSerPheLeuLeuArgLysGlyLysAspThrLeuGlu 212

478 TCAGCGAGGAATTCGCCACCAAAATTTTGGAGGAAAAAGTCAACGAGGGTGGT----- 531

213 LeuAlaArgGluPheAlaThrLysCysLeuGlnLysLysLeuAspGluGlyGlyAsnGlu 232

532 GTTGATGGGACCTTTTAAACAAGATCCGATATCTCTTTGGACATCCCTTCATTGAGGAG 591

233 IleAspGluAsnLeuLeuTrpIleArgHisSerLeuAspLeuProLeuHisTrpArg 252

592 ATTAAAAAGGCCAAATCGCCTGTGGGATCGAATGGTATAGGAAGAGCCCGACATGAAT 651

253 IleGlnSerValGluAlaArgTrpPheIleAspAlaTyrrAlaArgArgProAspMetAsn 272

652 CAGATGATGTGGACCTTGCCATATCGACATTAATATTGTTCAAGCACAATTTCAAGAA 711

273 ProLeuIlePheGluLeuAlaLysLeuAsnPheAsnIleIleGlnAlaThrHisGlnGln 292

712 GAGCTCAAGAATTCCTCAGGTGGTGGAGAAATACTGGGTTTGGTGGAGAGTGCCTTC 771

293 GluLeuLysAspLeuSerArgTrpSerArgLeuCysPheProGluLysLeuProPhe 312

772 GCAGGGATAGACTGGTGGATGCTACTTTTGGAACTATGGGATCATCGAGCCACGTCAAG 831

313 ValArgAspArgLeuValGlnSerPheMetTrpAlaValGlyMetPheGluProHisGln 332

832 CATGCAAGTGCAGGATATGATGGCGAAAGCAACGCTCTGATTACGGTGATTCGATGAT 891

333 HisGlyTyrrGlnArgLysMetAlaAlaThrIleIleValLeuAlaThrValIleAspAsp 352

892 ATTTATGATCTGTGGCACCTTAGAAGAACCTCGAACCAATTCACATGACCTCATTCGAA 951

353 IleTyrrAspValTyrrGlyThrLeuAspGluLeuGluLeuPheThrAspThrPheLysArg 372

952 TGGGATATAAACTCAATCGACCAACTCCCGATTACATGCAACTGTGCTTTCTTGCACTC 1011

373 TrpAspThrGluSerIleThrArgLeuProTyrrTyrrMetGluLeuCystyrrTrpGlyVal 392

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413 GlnTyrrLeuArgLysSerValValAspLeuValGluAlaTyrrPheHisGluAlaLysTrp 432

1132 TTCTACGGCGGCACAAACCAAGTTTGGAGAGTATTTCCGAAACATCATCGGACGTGATA 1191

433 TyrrHisSerGlyTyrrThrProSerLeuAspGluTyrrLeuAsnIleAlaLysIleSerVal 452

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453 AlaSerProAlaIleIleSerProTyrrTyrrPheThrPheAlaAsnAlaSerHisAspThr 472

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473 AlaValIleAspSerLeuTyrrGlnTyrrHisAspIleLeuCysLeuAlaGlyIleLeuLeu 492

1309 CGGCTTGCTGATGATTTGGAACTCGGTGGAAAGAGGTGAGCACAGGGATGTCGCGAAA 1368

493 ArgLeuProAspAspLeuGlyThrSerTyrrPheGluLeuAlaArgGlyAspValProLys 512

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1429 AAATGGCTGATAGCGGAGGTGTGGACAAGATGAATCGCGAGAGGGTGTGCAAGGATCTT 1488

533 LysPheLeuIleArgGluAlaTrpLysAspMetAsnThr---AlaIleAlaAlaGlyTyrr 551

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652	CCAGTAGTGTGGAGCTTGCCATACCTGCACCTTAAATATTGTTCAAGCAACAATTCAGAA	711
273	ProLeuIlePheGluLeuAlaLysLeuAsnPheAsnIleIleGlnAlaThrHisGlnGln	292
712	GAGCTCAAGAGATCCTTCAGGTGGTGGAGAAATACTGGGTTTGTGAGAAGCTGCCTTC	771
293	GluLeuLysAspLeuSerArgTrpTrpSerArgLeuCysPheProGluLysLeuProPhe	312
772	GCAAGGGATAGACTGGTGGAAATGCTACTTCTTGGAAATCTGGGATCATCGAGCGACGTGAG	831
313	ValArgAspArgLeuValGluSerPhePheTrpAlaValGlyMetPheGluProHisGln	332
832	CATGCAAGTGCAGGATAATGATGGCAAGTCAACGGCTCTCATTTACGGTGAATCGATGAT	891
333	HisGlyTyrGlnArgLysMetAlaAlaThrIleIleValLeuAlaThrValIleAspAsp	352
892	ATTATTGATGCTATGGCAACCTTAGAAGAACTCGAACCAATTCACTCACCTCATTCGAAAG	951
353	IleTyrAspValTyrGlyThrLeuAspGluLeuGluLeuPheThrAspThrPheLysArg	372
952	TGGGATATAAATCAATGACCAACTTCCCGATTACATGCACTGTGCTTCTTTCGCACATC	1011
373	TrpAspThrGluSerIleThrArgLeuProTyrTyrMetGlnLeuCysTyrTrpGlyVal	392
1012	AACAACCTTCGTGATACATCATCGTACGATGTTATTGAAGGAGAAAGCGCTCAACGTTATA	1071
393	HisAsnTyrIleSerAspAlaAlaTyrAspIleLeuLysGluHisGlyPheCysLeu	412
1072	CCCTACTCGGGCAATCGTGGGTGTGATTGGCGGATAAGTATATGTTAGAGCACCGCTGG	1131
413	GlnTyrLeuArgLysSerValValAspLeuValGluAlaTyrPheHisGluAlaLysTrp	432
1132	TTCTACGGCGGGCAACAAACCAAGTTTGGAAAGATATTTCGAGAACATCATCGGACGTGATA	1191
433	TyrHisSerGlyTyrThrProSerLeuAspGluTyrLeuAsnIleAlaLysIleSerVal	452
1192	AGTGGGCGCTGTATGTTAAGCCACATATCTCTCCGAGTAACAGAT---TCGTTCAACAAAG	1248
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1249	GAGACCGTCACAGTTGTGACAAATACCAAGATTTAGTTTCGTTGGTCATCCTTCGTTCTG	1308
473	AlaValIleAspSerLeuTyrGlnTyrHisAspIleLeuCysLeuAlaGlyIleIleLeu	492
1309	CGGCTTCTCATGATTGGGAACCTCGTGCGAAGAGGTGAGCAGAGGGATGTCGCGAA	1368
493	ArgLeuProAspAspLeuGlyThrSerTyrPheGluLeuAlaArgGlyAspValProLys	512
1369	TCATCTCAGTGTCTACGTAGCTACTCAATGCAATCGGAGCGGAGCGCGGAGCAACGCTG	1428
513	ThrIleGlnCysTyrMetLysGluThrAsnAlaSerGluGluGluAlaValGluHisVal	532
1429	AAATGGCTGATAGCGGAGGTGTGGAGCAAGATGAATCGCGAGAGGGGTGTGCAAGGATCT	1488
533	LysPheLeuIleArgGluAlaTrpLysAspMetAsnThr---AlaIleAlaAlaGlyTyr	551

QY	952	TGGGATATAAACTCAATGACCAACTTCCGATTACATGCAACTGTGCTTTCTTGCACTC	1011
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QY	1012	AACAATTCGTGATGATACATCGTACGATGTTATGAGGAGAAAGGCGTCACAGTTATA	1071
Db	393	HlsAsnTyrIleSerAspAlaIatyrAspIleLeuLysGluHisGlyPhePheCysLeu	412
QY	1072	CCCTACTCTCGGCAATCGTGGGTGTGATTGGGGGATAAGTATATGCTAGAGGCACGGTGG	1131
Db	413	GlnTyrLeuArgLysSerValValAspLeuValGluIatyrPheHisGluAlaLysTrp	432
QY	1132	TTCTACGGCGGGCACAAACCAAGTTTGGAGAGTATTTGGAGAACTCATGGCAGTCGATA	1191
Db	433	TyrHisSerGlyTyrThrProSerLeuAspGluTyrLeuAsnIleAlaLysIleSerVal	452
QY	1192	AGTGGGCGCTGTATGTTAAAGCAATATTTCTCCGAGTAACAGAT---	1248
Db	453	AlaserProAlaIleIleSerProThrTyrPheThrPheAlaAsnAlaSerHisAspThr	472
QY	1249	GAGACGTCGACAGTTGTGTAACAATACCAAGTATTAGTTGCTTGGTCATCTTCGTTCTG	1308
Db	473	AlaValIleAspSerLeuTyrGlnTyrHisAspIleLeuCysLeuAlaGlyIleIleLeu	492
QY	1309	CGCGTTCTGATGATTGGAACTCGTGGAAGAGGTGAGCAGACGGGATGTGCGGAAA	1368
Db	493	ArgLeuProAspAspLeuGlyThrSerTyrPheGluLeuAlaArgGlyAspValProLys	512
QY	1369	TCATCTCAGTGCTACATGACTGACTCAATGTCATCGAGCGGAGGCGCGGAAGCACGTG	1428
Db	513	ThrIleGlnCysTyrMetLysGluThrAsnAlaSerGluGluGluAlaValGluHisVal	532
QY	1429	AAATGGCTGATACGGAGGTGTGGACAAGATGAATCGCGAGAGGGGTGTGCAAGGATTCT	1488
Db	533	LysPheIleuIleArgGluAlatrpLysAspMetAsnThr---AlaIleAlaAlaGlyTyr	551

QY		1072	CCCTACCTGGCGCAATCGTGGGTGATTGTTGGGCGGATAAGTATATGTGTAGAGGCACGGTCG	1131
Db		413	GlutylLeuArgLysSerValValAspLeuValGluAlaTy:PheHisgLuAlaLysTp	432
QY		1132	TTCACGGCGGGCACAACCAAGTTTGGAAGAGTATTTCGAGAAGCATCGGCAGTCGATA	1191
Db		433	TyrHisSerGlyTyrThrProSerLeuAspGluTyrLeuAsnIleAlaLysIleSerVal	452
QY		1192	AGTGGGCCCTGTATGTAACGCACATATCTTCCTCCGAGTAACAGAT---TCGTTTCAAAAAG	1248
Db		453	AlaserProAlaIleIleserProThrTyrPheThrPheAlaasnaLaserHisaspThr	472
QY		1249	GAGACCGTCGACAGTTTGTAACAATACCAGATTTAGTTGCTGGTGGTCATCCTTCGTTCTG	1308
Db		473	AlavalIleaspSerLeuTyrGlnTyrHisaspIleLeuCysLeuAlaGlyIleIleLeu	492
QY		1309	CGGCTTCCTCAATGATTTGGAACTCGGTGGAGAGGTCGAGCAGAGGGGATGTCGCCGAAA	1368
Db		493	ArgLeuProaspAspleuGlyThrSerTyrPheIleuIleuAlargGlyaspValProLys	512
QY		1369	TCACTTCAGTGTCTACATGAGTCACTCAATGCATCGGAGCGGAGGCGCGGAAGCACGCTG	1428
Db		513	ThrilGlnCysTyrMetLysGluThrAsnAlaserGluGlucIuAlaValGluHuIseVal	532
QY		1429	AAATGGCTGTATAGCGGAGGTGTGGACAGACATGAATGTCGGAGAGGGGTGTTCGAAGGATTCT	1488
Db		533	LysPheLeuIleArgGluAlatrpLysaspMetAsnThr---AlaIleAlaAlaGlyTyr	551

413	GlutTyLeuArgLysSerValValAspLeuValGluAlaTyrPheHisGluAlaLysTyr	432
1132	TTCTACGGCGGGCACAACCAAGTTTGGAGAGTATTTGGAGAACTCATGGCAGTCGATA	1191
433	TyrHisSerGlyTyrThrProSerLeuAspGluTyrLeuAsnIleAlaLysIleSerVal	452
1192	AGTGGGCGCTGTATGTAACGCACATATCTTCCGAGTAACAGAT---TCGTTCAAAAG	1248
453	AlaSerProAlaIleIleSerProThrTyrPhePheAlaAsnAlaSerHisAspThr	472
1249	GAGACCGTGACAGTTGTACAAATACAGGATTAGTTGCTGTGGTCATCCTTCGTTCTCG	1308
473	AlaValIleAspSerLeuTyrGlnTyrHisAspIleLeuCysLeuAlaGlyIleIleLeu	492
1309	CGGCTTGCTCATATTGGGAACCTCGTGCGAAGAGGTGAGCAGAGGGGATGTGCCGAAA	1368
493	ArgLeuProAspAspLeuGlyThrSerTyrPheGluLeuAlaArgGlyAspValProLys	512
1369	TCATCTCAGTGTCTACATGAGTCACTCAATGCATCGAGCGGAGCGCGCGAAGCAGCTGT	1428
513	ThrIleGlnCysTyrMetLysGluThrAsnAlaSerGluGluGluAlaValGluHisIleVal	532
1429	AAATGGCTGTATAGCGGAGGTGTGGACAGACATGAATCGCGGAGGGGTGTGCGAGGATTCT	1488
533	LysPheIleuIleArgGluAlaTyrLysAspMetAsnThr---AlaIleAlaAlaGlyTyr	551

Qy 1489 CCATTGCGCAAGATTTTATAGGATGTCAGTTGATTAGGAGGATGCGCAGTTGATG 1548
Db 552 ProPheProaspGlyMetValalaglyAlaalaasnilleGlyargvalAlaGlnPheile 571
Qy 1549 TACCATAATGAGATGGCGCAGGACACACACACCTTATATACATCAACAATGACACAGA 1608
Db 572 TyrLeuHisGlyaspGlyPheGlyValGlnHisSerlysthrTyrGluHisileAlagly 591
Qy 1609 ACCTTATTCGAGCCCTTGGCA 1629
Db 592 LeuLeuPheGluProTyrAla 598
RESULT 12
US-09-903-012-26
; Sequence 26 Application US/09903012
; Patent No. US2002094557A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US2002094557A1, Joseph P.
; APPLICANT: Starks, Courtney M.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903.012
; CURRENT FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Salvia officinalis
US-09-903-012-26
Alignment Scores:
Pred. No.: 3,49e-128 Length: 598
Score: 1468.00 Matches: 281
Percent Similarity: 71.12% Conservative: 108
Best Local Similarity: 51.37% Mismatches: 152
Query Match: 50.48% Indels: 6
DB: 9 Gaps: 5
US-09-938-956-6 (1-1632) x US-09-903-012-26 (1-598)
Qy 1 ATGAGACGATCCGAAACTACAACTTCTCGTTGGGATGTCACATTCATCCCAATCGCTT 60
Db 54 IleargSerGlyAsnTyrGlnProAlaLeuTrpAspSerAsnTyrIleGlnSerLeu 73
Qy 61 CTCAGTACTATAAGGAGGACAAACAGTATTAGGCTTCTGAGCTGGTCACTTTGGTG 120
Db 74 AsnThrProTyrThrGluGluArgHisLeuAspArgLysAlaGluLeuIleValGlnVal 93
Qy 121 AAGATGGAACTCGGAGAAACGATCAAACTTCGACAACTTGATTCATCGATGACTTG 180
Db 94 ArgileLeuLeuLysGluLysMetGluProValGlnGlnLeuGluLeuIleHisAspLeu 113
Qy 181 CAGAGATGGGGCTGTCGATCATTCCAAATGATTCAGTTCAGAAAGAACTTGTCTCTATA 240
Db 114 LysTyrLeuGlyLeuSerAspPhePheGlnAspGluLeuLysGluIleLeuGlyValile 133
Qy 241 TATCTCGACCATCACTATTACAAAGCCCTTTTCCAAAAGAAAGAGGAGTCTCTACTCC 300
Db 134 TyrAsnGluHisLysCysPheHisAsnAsn---GluValGluLysMetAspLeuTyrPhe 152
Qy 301 ACATCTCTTGCTATAGGCTCCTCAGAGAACATGGTTTTCAAGTCGCACAGAGGTATTC 360

Db 153 ThrAlaLeuGlyPheArgLeuLeuArgGlnHisGlyPheAsnIleSerGlnAspValPhe 172
Qy 361 GATAGTTTCAGAAACGAGAGGGT---GAGTTCAGAAAGAGCCTTAGCGACACACAGAGA 417
Db 173 AnCysPheLysAsnGluLysGlyIleAspPheLysAlaSerLeuAlaGlnAspThrLys 192
Qy 418 GGATTGTTGCAACTGTATGAGCTTCCCTTCTGTTGAGCGAAGGCGAAACACACGCTCGAG 477
Db 193 GlyMetLeuGlnLeuTyrGluAlaSerPheLeuLeuArgLysGlyGluAspThrLeuGlu 212
Qy 478 TCAGCGAGGGAATTCGCCACCAAAATTTTGGAGGAAAAGTGAACGAGGGTGGT----- 531
Db 213 LeuAlaArgGluPheAlaThrLysCysLeuGlnLysLysLeuAspGluGlyLysAsnGlu 232
Qy 532 GTTGATGGCGACCTTTTACAGAAATCGCATATCTTTGGACATCCCTCTTTCATTGGAGG 591
Db 233 IleAspGluAsnLeuLeuLeuTrpIleArgHisSerLeuAspLeuProLeuHisTrpArg 252
Qy 592 ATTAAGGCGCAAAATGCACACTGTGTGATCGAATCGTATAGGAAGGCGCCGACATGAAT 651
Db 253 IleGlnSerValGluAlaArgTrpPheIleAspAlaTyrAlaArgArgProAspMetAsn 272
Qy 652 CCAGTAGTGTGGAGCTTGCCTACTCGACITTAATATTGTTTCAGACCAAAATTTCAAGAA 711
Db 273 ProLeuIlePheGluLeuAlaLysLeuAsnPheAsnIleIleGlnAlaThrHisGlnGln 292
Qy 712 GAGCTCAAGAAATCCTTCAGGTGGTGGAGAAATACTGGGTTTGTTCAGAAAGTGGCTTC 771
Db 293 GluLeuLysAspLeuSerArgTrpSerArgLeuCysPheProGluLysLeuProPhe 312
Qy 772 GCAAGGATAGACTGGTGGATGCTACTTTTGGATATCTGGATCATCGACGACGTCAG 831
Db 313 ValArgAspArgLeuValGluSerPhePheTrpAlaValGlyMetPheGluProHisGln 332
Qy 832 CATGCAAGTGCAGGATATGATGGCAAGTCAACGCTCTGATTACGTCGTCATGATGAT 891
Db 333 HisGlyTyrGlnArgLysMetAlaAlaThrIleIleValLeuAlaThrValIleAspAsp 352
Qy 892 ATTTATGATGTTATGGACCTTAGAAGAACTCGCAAAATTTCACTGACCTCATTCGAAGA 951
Db 353 IleTyrAspValTyrGlyThrLeuAspGluLeuGluLeuPheThrAspThrPheLysArg 372
Qy 952 TGGGATATAAACTCAATCGACCACTTCCGATATACATGCAACTGCTGCTTCTTGCACCTC 1011
Db 373 TrpAspThrGluSerIleThrArgLeuProTyrTyrMetGlnLeuCysTyrTrpGlyVal 392
Qy 1012 AACAACTTCGTCGATGATACATCGTACGATGTTATGAAGGAGAAAGGCGTCAACGTTATA 1071
Db 393 HisAsnTyrIleSerAspAlaAlaTyrAspIleLeuLysGluHisGlyPhePheCysLeu 412
Qy 1072 CCTTACCTCGGCAATCGTGGTGTGATTTGGCGGATAAGTATATGATGAGGACCGGTGG 1131
Db 413 GlnTyrLeuArgLysSerValValAspLeuValGluAlaTyrPheHisGluAlaLysTrp 432
Qy 1132 TTCTACGGCGGCACAAACAAAGTTTGGAAAGTATTTGGAGAACTCATGGCAGTCGATA 1191
Db 433 TyrHisSerGlyTyrThrProSerLeuAspGluTyrLeuAsnIleAlaLysIleSerVal 452
Qy 1192 AGTGGCCCTGTATGTTAAGCGACATATCTTCCAGTAACAGAT---TCGTTCCACAAAG 1248
Db 453 AlaSerProAlaIleIleSerProThrTyrPheThrPheAlaAsnAlaSerHisAspThr 472
Qy 1249 GAGACCGTCGACAGTTTGTACAAATACCAACGATTTAGTTTGGTTCATCCCTCGTCTCG 1308
Db 473 AlaValIleAspSerLeuTyrGlnTyrHisAspIleLeuCysLeuAlaGlyIleLeuLeu 492
Qy 1309 CGGCTTGTGATGATTTGGGAACTCGGTGGAGAGGTGACGAGAGGGATGTGCGGAA 1368
Db 493 ArgLeuProAspAspLeuGlyThrSerTyrPheGluLeuAlaArgGlyAspValProLys 512
Qy 1369 TCACCTTCAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1428

Db 513 ThrIleGlnCysTyrMetLysGluThrAsnAlaSerGluGluAlaValGluHisVal 532
 QY 1429 AAATGGCTGATCGGAGGTGGAGAGATCAATGCGGAGAGGGTGTGAGAGATTCT 1488
 Db 533 LysPheLeuIleArgGluAlaTrpLysAspMetAsnThr- --AlaIleAlaAlaGlyTyr 551
 QY 1489 CCATTCGGCAAGATTTTATAGGATGTGCAGTTGATTTAGGAGGATGCGCGAGTTGATG 1548
 Db 552 PropheProAspGlyMetValAlaGlyAlaAlaAsnIleGlyArgValAlaGlnPheIle 571
 QY 1549 TACCATAATGGAGTGGGACGGCACACACACCCCTATTATACATCAACAATGACCCAGA 1608
 Db 572 TyrLeuHisGlyAspGlyPheGlyValGlnHisSerLysThrTyrGluHisIleAlaGly 591
 QY 1609 ACCTTATTCGAGCCCTTTGCA 1629
 Db 592 LeuLeuPheGluProTyrAla 598

RESULT 13

US-09-900-797-26
 ; Sequence 26, Application US/09900797
 ; Publication No. US20030087406A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chappell, Joseph
 ; APPLICANT: No. US20030087406A1, Joseph P.
 ; APPLICANT: Stark, Courtney M.
 ; APPLICANT: Manna, Kathleen R.
 ; TITLE OF INVENTION: SYNTHASES
 ; FILE REFERENCE: 07678-025001
 ; CURRENT APPLICATION NUMBER: US/09/900,797
 ; CURRENT FILING DATE: 2001-07-06
 ; PRIORITY APPLICATION NUMBER: US/09/398,395
 ; PRIORITY FILING DATE: 1999-09-17
 ; PRIORITY FILING DATE: 1999-04-22
 ; PRIORITY FILING DATE: 1999-08-23
 ; NUMBER OF SEQ ID NOS: 58
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 26
 ; LENGTH: 598
 ; TYPE: PRT
 ; ORGANISM: Salvia officinalis
 US-09-900-797-26

Alignment Scores:
 Pred. No.: 3,496-128 Length: 598
 Score: 1468.00 Matches: 281
 Percent Similarity: 71.12% Conservative: 108
 Best Local Similarity: 51.37% Mismatches: 152
 Query Match: 50.48% Indels: 6
 DB: 10 Gaps: 5

US-09-938-956-6 (1-1632) x US-09-900-797-26 (1-598)

QY 1 ATGAGACGATCCGGAACATCAACCCCTTCCTGCGGATGTCAACTTCATCAATCGCTT 60
 Db 54 IleArgSerGlyAsnTyrGlnProAlaLeuTrpAspSerAsnTyrIleGlnSerLeu 73
 QY 61 CTCAGTGACTATAAGGAGGACAAACACGTTAGGCTTCCTGAGCTGTGCTTGGTG 120
 Db 74 AsnThrProTyrThrGluGluArgHisLeuAspArgLysAlaGluLeuIleValGlnVal 93
 QY 121 AAGATGGAACTGGAGAAAGACGGATCAATTCGACAACTTGAGTTGATCGATGACTTG 180
 Db 94 ArgIleLeuLeuLysGluLysMetGluProValGlnGlnLeuLeuIleHisAspLeu 113
 QY 181 CAGAGGATGGGCTGCTCCATCATTTCCAAATGATGATTCAGAAATCTTGTCTCTATA 240
 Db 114 LysTyrLeuGlyLeuSerAspPheGlnAspGluIleLysGluIleLeuGlyValIle 133
 QY 241 TATCTCGACCATCACTATTACAGAACCCCTTTTCCAAAGAGAAAGGAGTCTTACTCC 300

Db 134 TyrAsnGluHisLysCysPheHisAsnAsn- --GluValGluLysMetAspLeuTyrPhe 152
 QY 301 ACATCTCTTCATTTAGGCTCCTCAGAGAACATGGTTTCAATGCGCACAGAGAGTATTC 360
 Db 153 ThrAlaLeuGlyPheArgLeuLeuArgGlnHisGlyPheAsnIleSerGlnAspValPhe 172
 QY 361 GATAGTTTCAAGAACGAGGAGGGT- --GACTTCAAAAGAAAGCCTTAGCGACGACACAGA 417
 Db 173 AsnCysPheLysAsnGluLysGlyIleAspPheLysAlaSerLeuAlaGlnAspThrLys 192
 QY 418 GGAATTTGCACTGATGATGAGCTTCTCTTCTGACGGAAGCGGAAACCAACGCTCGAG 477
 Db 193 GlyMetLeuGlnLeuTyrGluAlaSerPheLeuLeuArgLysGlyLeuAspThrLeuGlu 212
 QY 478 TCAGCGAGGGAATTCGCCCAAAATTTTGGAGAAAAGTGAACGAGGGTGGT- -- 531
 Db 213 LeuAlaArgGluPheAlaThrLysCysLeuGlnLysLysLeuAspGluGlyAsnGlu 232
 QY 532 GTTGATGGCGACCTTTTAAACAAGATCGCATATCTTTGGACATCTCTCTCTTCAATTGAGG 591
 Db 233 IleAspGluAsnLeuLeuTrpIleArgHisSerLeuAspLeuProLeuHisTrpArg 252
 QY 592 ATTAAAGGCGCAATCGACCTGTGTGATCGAATGTATAGGAGAGGCGCCGACATGAAT 651
 Db 253 IleGlnSerValGluAlaArgTrpPheIleAspAlaTyrAlaArgArgProAspMetAsn 272
 QY 652 CCAGTAGTGTGGAGCTGCCATCTACCTACTTTTGGAAATCTGGGATCATCGACCCAGCTCAG 831
 Db 313 ValArgAspArgLeuValGluSerPhePheTrpAlaValGlyMetPheGluProHisGln 332
 QY 832 CATGCAAGTCAAGGATATGATGGGCAAGTCAACGCTCTGATTACGCTGATCGATGAT 891
 Db 333 HisGlyTyrGlnArgLysMetAlaIleThrIleValLeuAlaThrValIleAspAsp 352
 QY 892 ATTTATGATGCTATGGCACCCTTAGAAGAACTCGAAACAATTCACCTGACCTCATTCGAAGA 951
 Db 353 IleTyrAspValTyrGlyThrLeuAspGluLeuGluLeuPheThrAspThrPheLysArg 372
 QY 952 TGGGATATAAACTCAATCGACCACTCCGATTAATCATGCACTGTGCTTCTTGTGACTC 1011
 Db 373 TrpAspThrGluSerIleThrArgLeuProTyrTyrMetGlnLeuCysTyrTrpGlyVal 392
 QY 1012 AACAACTTCGTGATCATCATCGTACGATGTTTATCAAGGAGAAAGCGCTCAACGTTATA 1071
 Db 393 HisAsnTyrIleSerAspAlaIleTyrAspIleLeuLysGluHisGlyPhePheCysLeu 412
 QY 1072 CCCTACTGCGCAATCGTGGTGGTGGTGGGATAGTATATATGATGAGGACCGGTGG 1131
 Db 413 GlnTyrLeuArgLysSerValValAspLeuValGluAlaTyrPheHisGluAlaLysTrp 432
 QY 1132 TTCTAGCGGGGACAAACCAAGTTTGGAGAGATATTTCGAGAACTCATGCGAGTGCATA 1191
 Db 433 TyrHisSerGlyTyrThrProSerLeuAspGluTyrLeuAsnIleAlaLysIleSerVal 452
 QY 1192 AGTGGGCCCTGTATGTAAACGACATATCTTCCGAGTAAACAGAT- --TCGTTCAACAAG 1248
 Db 453 AlaSerProAlaIleIleSerProThrTyrPheThrPheAlaAsnAlaSerHisAspThr 472
 QY 1249 GAGACGCTGACAGTTGTACAAATACCAACGATTTAGTTGGTGGTTCATCTTCTGTTCTG 1308
 Db 473 AlaValIleAspSerLeuTyrGlnTyrHisAspIleLeuCysLeuAlaGlyIleIleLeu 492
 QY 1309 CGGCTTCTGATGATTTGGGAACCTCGGTGGAGAGGTGAGGAGGAGGTGTCGCGAA 1368
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Qy 1369 TCAGTTCAGTGTACATGATGTGACTCAATGCAATCGGAGCGGAGCGCGGAGCAACGCTG 1428

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Qy 1429 AAATGGCTGATAGCGGAGGTGTGGAAGAAGATGAATGCGGAGAGGGGTGTGGAAGGATTCT 1488

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Qy 1489 CCATTCGGCAAAAGATTTTATAGGATGTGCAGTTGATTTAGGAAGGATGGCGCATGTGATG 1548

Db 552 ProPheProaspGlyMetValAlaGlyAlaAlaAsnIleGlyArgValAlaGlnPheIle 571

Qy 1549 TACCATAATGGAGATGGCGCGGCACACACACCTATTATACATCAACAATGACCAGA 1608

Db 572 TyrLeuHisGlyaspGlyPheGlyValGlnHisSerLysThrTyrGluHisIleAlaGly 591

Qy 1609 ACCTATTTCAGCCCTTTGCA 1629

Db 592 LeuLeupheGluProTyrAla 598

RESULT 14

US-09-887-586A-32

; Sequence 32, Application US/09887586A

; Patent No. US20020094556A1

; GENERAL INFORMATION:

; APPLICANT: Chappell, Joseph

; APPLICANT: No. US20020094556A11, Joseph P.

; APPLICANT: Starks, Courtney M.

; APPLICANT: Manna, Kathleen R.

; TITLE OF INVENTION: SYNTHASES

; FILE REFERENCE: 07678-025001

; CURRENT APPLICATION NUMBER: US/09/887,586A

; CURRENT FILING DATE: 2001-06-22

; PRIOR APPLICATION NUMBER: 09/398,395

; PRIOR FILING DATE: 1999-09-17

; PRIOR APPLICATION NUMBER: 60/130,628

; PRIOR FILING DATE: 1999-04-22

; PRIOR APPLICATION NUMBER: 60/150,262

; PRIOR FILING DATE: 1999-08-23

; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 32

; LENGTH: 556

; TYPE: PRT

; ORGANISM: Solanum tuberosum

US-09-887-586A-32

Alignment Scores:

Pred. No.: 5,08e-69 Length: 556

Score: 836.00 Matches: 182

Percent Similarity: 54.68% Conservative: 116

Best Local Similarity: 33.39% Mismatches: 207

Query Match: 28.75% Indels: 40

DB: 9 Gaps: 10

US-09-938-956-6 (1-1632) x US-09-887-586A-32 (1-556)

Qy 1 ATGAGACGATCGGAAACTCAACACCTTCTCGTTGGGATGTCAACTTCATCCAAATCGCTT 60

Db 17 ValArgProIleAlaAspPheSerProSerLeuTrpGlyAspArgPheHisSerPheSer 36

Qy 61 CTCAGTGTACTAAGGAGGACAAACAGTGTAGGGCTTCTGAGCTGGTGGTCTGGTGGT 120

Db 37 LeuAspAsnGlnIleAlaGlyLysTyr-----AlaGlnGluIleGluThrLeu--- 52

Qy 121 AAGATGGAAGTGGAGAAAGAAACCGATCAAAAT----- 153

Db 53 -----LysGluLysSerArgIleIleLeuSerAlaSerArgArgThr 67

Qy 154 -----CGACAACTTGATTCGATCGATCGATTCGAGAGATGGGGCTGTCGATCATTC 207

Db 68 LeuAlaGluLysLeuAspLeuIleAspIleValGluArgLeuGlyIleAlaTyrHisPhe 87

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QY 1273 TACCAGATTAGTTCGTTGGTCATCCCTCGTTCGGCTGCTGATGATTTGGGAACC 1332
Db      :      :      :      :      :      :      :      :      :
437 AsnProLysLeuLeuGluAlaAsnValThrLeuCysArgValIleAspPileAlaThr 456
QY 1333 TCGTGGGAAGAGTGCAGCAGAGCGGATGTGCCGAATCACTTCAGTCTACATGAGTAC 1392
Db      :      :      :      :      :      :      :      :      :
457 TyrGluValGluLysGlyArgGlyGlnIleAlaThrGlyIleGluCysTyrMetArgAsp 476
QY 1393 TACAATGCATCGAGCGGAGCGGAGGAGGAGCAGCGTGAATCGCTGATAGCGGAGTGTGG 1452
Db      :      :      :      :      :      :      :      :      :
477 TyrGlyValSerThrGluLysAlaMetGluLysPheGlnGluMetAlaGluThrAlaTyr 496
QY 1453 AAGAAGATCAATCGCGAGAGGAGTGTCCGAAGGATTCCTCCATCGCAAGATTTTATAGGA 1512
Db      :      :      :      :      :      :      :      :      :
497 LysAspValAsn--GluGlyIleLeuArgProThrProValSerThrGluIleLeuThr 515
QY 1513 TGTGCAGTTCATTTAGGAAGATGCGCGAGTGTATGATAC---CATATGAGATGGGCAC 1569
Db      :      :      :      :      :      :      :      :      :
516 ArgIleLeuAsnLeuAlaArgIleIleAspValThrTyrLysHisAsnGlnAspGlyTyr 535
QY 1570 GGCACACACACCCCT 1584
Db      :      :      :      :      :      :      :      :      :
536 -----ThrHisPro 538

RESULT 15
US-09-903-012-32
; Sequence 32, Application US/09903012
; Patent No. US20020094557A1
; GENERAL INFORMATION:
; APPLICANT: Chappell, Joseph
; APPLICANT: No. US20020094557A1, Joseph P.
; APPLICANT: Starks, Kathleen R.
; APPLICANT: Manna, Kathleen R.
; TITLE OF INVENTION: SYNTHASES
; FILE REFERENCE: 07678-025001
; CURRENT APPLICATION NUMBER: US/09/903,012
; PRIOR FILING DATE: 2001-07-11
; PRIOR APPLICATION NUMBER: 09/398,395
; PRIOR FILING DATE: 1999-09-17
; PRIOR APPLICATION NUMBER: 60/100,993
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/130,628
; PRIOR FILING DATE: 1999-04-22
; PRIOR APPLICATION NUMBER: 60/150,262
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ IDS NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Solanum tuberosum
US-09-903-012-32

Alignment Scores:
Pred. No.: 5,08e-69 Length: 556
Score: 836.00 Matches: 182
Percent Similarity: 54.68% Conservative: 116
Best Local Similarity: 33.39% Mismatches: 207
Query Match: 28.75% Indels: 40
DB: 9 Gaps: 10

US-09-938-956-6 (1-1632) x US-09-903-012-32 (1-556)
QY 1 ATGAGACGATCGGAAGACTACACCTTCGTTGGATGTCACCTTCATCCATCGCTT 60
Db      :      :      :      :      :      :      :      :      :
17 ValArgProIleAlaAspPheSerProSerLeuTyrPglyAspArgPheHisSerPheSer 36
QY 61 CTCAGTGCATATAAGGAGGACAAACAGCTGATTAGGCTTCCTCAGCTGGTCACTTTGGTG 120
Db      :      :      :      :      :      :      :      :      :
37 LeuAspAsnGlnIleAlaGlyLysTyr-----AlaGlnGluIleGluThrLeu--- 52
QY 121 AAGATGCGACTGGGAAGAAACCGATCAAAATTT----- 153
Db      :      :      :      :      :      :      :      :      :

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53 -----LysGluGlnSerArgIleIleLeuSerAlaSerSerArgArgThr 67
154 -----CGACAACTGAGTTGATCGACTTCGAGAGGATGGGCTGTCGATCATTTTC 207
Db      :      :      :      :      :      :      :      :      :
68 LeuAlaGluLysLeuAspLeuIleAspIleValGluArgLeuGlyIleAlaTyrHisPhe 87
QY 208 CAAATGAGTTCAAAGAAATCTTCTCTCTATATAT-----CTCGACCAT 252
Db      :      :      :      :      :      :      :      :      :
88 GluLysGlnIleAspAspMetLeuAspGlnPheTyrLysAlaAspProAsnPheGluAla 107
QY 253 CACTATTACAAGACCCCTTTTCCAAAAGAAAGGATCTCTACTCCACATCTCTTCCA 312
Db      :      :      :      :      :      :      :      :      :
108 HisGluTyr-----AsnAspLeuGlnThrLeuSerValGln 119
QY 313 TTTAGCTCTCCAGAACATGTTTTCAGATCGCACAGAGGATTTTCGATAGTTTCAAG 372
Db      :      :      :      :      :      :      :      :      :
120 PheArgLeuLeuArgGlnHisGlyTyrAsnIleSerProLysLeuPheIleArgPheGln 139
QY 373 AACGAGAGGAGTTCAGAAAGCCTTAGCGAGACACACAGAGGATTTGTCACACTG 432
Db      :      :      :      :      :      :      :      :      :
140 AspAlaLysGlyLysPheLysGluSerLeuLysPheLysGlyLeuLeuAsnLeu 159
QY 433 TATGAAGCTTCCTTCTGTTGACGGAAGCGAAACACACGCTCGAGTCAGCGAGGAATTC 492
Db      :      :      :      :      :      :      :      :      :
160 TyrGluAlaSerHisValArgThrHisGlyGluAspIleLeuGluGluAlaLeuAlaPhe 179
QY 493 GCCACCAATTTTGGAGGAAAGTCAACGAGGGTGTGTTGATGGCGACCTTTTAAACA 552
Db      :      :      :      :      :      :      :      :      :
180 SerThrAlaHisLeuGluSerAlaAlaProHis-----LeuLysSerProLeuSerLys 197
QY 553 AGAATCCGATATCTTTGGACATCCCTCTTCATTGGAGGATTTAAAGGCCAAATGCACCT 612
Db      :      :      :      :      :      :      :      :      :
198 GlnValThrHisAlaLeuGluGlnSerLeuHisLysSerIleProArgValGluThrArg 217
QY 613 GTGTGGATCGAATGGTATAGGAAGCGCCGACATCAATCCAGTACTGTGGAGCTTGC 672
Db      :      :      :      :      :      :      :      :      :
218 TyrPheIleSerIleTyrGluGluGluGlnLysAsnAspValLeuLeuGlnPheAla 237
QY 673 ATACTCGACTTAATATTTGTCAGACCAATTTCAAGAAGAGCTCAAGAATCTTCAG 732
Db      :      :      :      :      :      :      :      :      :
238 LysLeuAspPheAsnLeuLeuGlnMetLeuHisLysGlnGluLeuSerGluValSerArg 257
QY 733 TGTGGAGAAATCTGGTTTGTGAGAGCTGCCCTTCGCAAGGAGATAGCTGTGGA 792
Db      :      :      :      :      :      :      :      :      :
258 TrpTrpLysAspLeuAspPheValThrLeuProTyrAlaArgAspArgAlaValGlu 277
QY 793 TGCTACTTTTGGAAATCTGGATCATCGAGCCACCGTCAGCATCGCAAGTCAAGGATAATG 852
Db      :      :      :      :      :      :      :      :      :
278 CysTyrPheTrpThrMetGlyValTyrAlaGluProGlnTyrSerGlnAlaArgValMet 297
QY 853 ATGGGCAAGTCACGCTCTGATTACGGTGCATGATATTATGATCTCTATCGCACC 912
Db      :      :      :      :      :      :      :      :      :
298 LeuAlaLysThrIleAlaMetIleSerIleValAspAspThrPheAspAlaTyrGlyIle 317
QY 913 TTAGAAGAACTCGAACAAATTCACCTGACCTCATTCGAAGATGGGATATAAATCAATCGAC 972
Db      :      :      :      :      :      :      :      :      :
318 ValLysGluLeuGluIleTyrThrAspAlaIleGlnArgTrpAspIleSerGlnIleAsp 337
QY 973 CAATCTCCCATTCATGCACTGCTCTTCTGCACTCAACACTTCGTCGATGATACA 1032
Db      :      :      :      :      :      :      :      :      :
338 ArgLeuProAspLysMetLysIleSerTyrLysAlaLeuLeuAspLeuTyrAsnAspTyr 357
QY 1033 TCGTACGATGTTAAGAGGAGAAAGCGTCAACGTTATACCTTACCTCGGCAATCGTGG 1092
Db      :      :      :      :      :      :      :      :      :
358 GluMetGluLeuSerLysAspGlyArgSerAspValValHisTyrAlaLysGluArgMet 377
QY 1093 GTTGATTGGCGGATTAAGTATATGTTAGAGGACCGTGGTCTTACGGGGGACAAACA 1152
Db      :      :      :      :      :      :      :      :      :
378 LysGluIleValArgAsnTyrPheValGluAlaLysTrpPheIleGluGlyTyrMetPro 397
QY 1153 AGTTTGAAGAGATTGTTGAGAACTCATGGCAGTGCATTAAGTGGGCCCTGTATGTTAACG 1212
Db      :      :      :      :      :      :      :      :      :
398 ProValSerGluTyrLeuSerAsnAla---LeuAlaThrSerThrTyrTyrLeuLeuThr 416

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QY 1213 CACATATTCTTCGAGTAACAGATTGTTTCAAAAGGAGACGTCGACAGATTGTACAAA 1272
Db   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
417 ThrThrSerTyrLeuGlyMetLysSerAlaAsnLysGlnAspPheGluTrpLeuAlaLys 436

QY 1273 TACCAGATTAGTTCGTTGGTCATCCCTTCGTTCTGCGCTTGCTGATGATTGGGAACC 1332
Db   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
437 AsnProLysIleLeuGluAlaAsnValThrLeuCysArgValIleAspAspIleAlaThr 456

QY 1333 TCGGTGGAAGAGGTGAGCAGAGGGGATGTGCCGAAATCACTTCAGTGTACATGAGTGAC 1392
Db   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
457 TyrGluValGluLysGlyArgGlyGlnIleAlaThrGlyIleGluCysTyrMetArgAsp 476

QY 1393 TACAATGCATCGAGCGGAGCGCGGAAAGCAGCAGGTGAATGCTGATAGCGAGGTGG 1452
Db   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
477 TyrGlyValSerThrGluLysAlaMetGluLysPheGlnGluMetAlaGluThrAlaTrp 496

QY 1453 AAGAAGATGAATCGGAGAGGGGTGTCGAAAGGATTCCTCAATTCGCAAGATTTTATAGGA 1512
Db   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
497 LysAspValAsn---GluGlyIleLeuArgProThrProValSerThrGluIleLeuThr 515

QY 1513 TGTGCAGTTGATTAGGAAGGATGGCGCAGTTGATGTAC---CATAATGGAGATGGCAC 1569
Db   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
516 ArgIleLeuAsnLeuAlaArgIleIleAspValThrTyrLysHisAsnGlnAspGlyTyr 535

QY 1570 GGCACACACACACCT 1584
Db   :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
536 -----ThrHisPro 538

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Search completed: March 18, 2004, 06:18:30
Job time : 100.5 secs